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RAW SEQUENCE LISTING

DATE: 09/07/2001

PATENT APPLICATION: US/09/933,814

TIME: 16:44:13

Input Set : A:\Wallach16B.txt

Output Set: N:\CRF3\09072001\I933814.raw

ENTERED

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3 <110> APPLICANT: WALLACH, David
4     BOLDIN, Mark
5     VARFOLOMEEV, Eugene
6     METT, Igor
8 <120> TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS/APOL RECEPTORS
10 <130> FILE REFERENCE: WALLACH-16B
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/933,814 0 ✓
C--> 12 <141> CURRENT FILING DATE: 2001-08-22
12 <150> PRIOR APPLICATION NUMBER: 08/860,082
13 <151> PRIOR FILING DATE: 1997-08-19
15 <150> PRIOR APPLICATION NUMBER: PCT/US95/16542
16 <151> PRIOR FILING DATE: 1995-12-14
18 <150> PRIOR APPLICATION NUMBER: IL 112022
19 <151> PRIOR FILING DATE: 1994-12-15
21 <150> PRIOR APPLICATION NUMBER: IL 112692
22 <151> PRIOR FILING DATE: 1995-02-19
24 <160> NUMBER OF SEQ ID NOS: 2
26 <170> SOFTWARE: PatentIn version 3.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 1701
30 <212> TYPE: DNA
31 <213> ORGANISM: Homo sapiens
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (1)..(768)
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39 Val Asn Gln Ala Pro Glu Cys Arg Phe Gly Gly Gly Ile Leu Gly Pro
40 1      5      10      15
42 ctg ggc aag cgg cga gac ctg gcc agg gcc agc gag ccg agg aca gag      96
43 Leu Gly Lys Arg Arg Asp Leu Ala Arg Ala Ser Glu Pro Arg Thr Glu
44      20      25      30
46 ggc gcg cgg agg gcc ggg ccg cag ccc cgg ccg ctt gca gac ccc gcc      144
47 Gly Ala Arg Arg Ala Gly Pro Gln Pro Arg Pro Leu Ala Asp Pro Ala
48      35      40      45
50 atg gac ccg ttc ctg gtg ctg ctg cac tcg gtg tcg tcc agc ctg tcg      192
51 Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser Ser Leu Ser
52      50      55      60
54 agc agc gag ctg acc gag ctc aag ttc cta tgc ctc ggg cgc gtg gtc      240
55 Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly Arg Val Val
56 65      70      75      80
58 aag cgc aag ctg gag cgc gtg cag agc ggc cta gac ctc ttc tcc atg      288
59 Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu Phe Ser Met
60      85      90      95
62 ctg ctg gag cag aac gac ctg gag ccc ggg cac acc gag ctc ctg cgc      336
63 Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu Leu Leu Arg
64      100      105      110

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66 gag ctg ctc gcc tcc ctg cgg cgc cac gac ctg ctg cgg cgc gtc gac      384
67 Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg Arg Val Asp
68      115      120      125
70 gac ttc gag gcg ggg gcg gcc ggg gcc gcg cct ggg gaa gaa gac      432
71 Asp Phe Glu Ala Gly Ala Ala Ala Gly Ala Ala Pro Gly Glu Glu Asp
72      130      135      140
74 ctg tgt gca gca ttt aac gtc ata tgt gat aat gtg ggg aaa gat tgg      480
75 Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly Lys Asp Trp
76 145      150      155      160
78 aga agg ctg gct cgt cag ctc aaa gtc tca gac acc aag atc gac agc      528
79 Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys Ile Asp Ser
80      165      170      175
82 atc gag gac aga tac ccc cgc aac ctg aca gag cgt gtg cgg gag tca      576
83 Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val Arg Glu Ser
84      180      185      190
86 ctg aga atc tgg aag aac aca gag aag gag aac gca aca gtg gcc cac      624
87 Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr Val Ala His
88      195      200      205
90 ctg gtg ggg gct ctc agg tcc tgc cag atg aac ctg gtg gct gac ctg      672
91 Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val Ala Asp Leu
92      210      215      220
94 gta caa gag gtt cag cag gcc cgt gac ctc cag aac agg agt ggg gcc      720
95 Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg Ser Gly Ala
96 225      230      235      240
98 atg tcc ccg atg tca tgg aac tca gac gca tct acc tcc gaa gcg tcc      768
99 Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser Glu Ala Ser
100      245      250      255
102 tgatgggccc ctgctttgcg ctggtggacc acaggcatct acacagcctg gactttggtt      828
104 ctctccagga aggtagccca gcaactgtgaa gacccagcag gaagccaggc tgagtgagecc      888
106 acagaccacc tgcttttgaa ctcaagctgc gtttattaat gcctctcccg caccaggccg      948
108 ggcttggggc ctgcacagat atttccattt ctctctcact atgacactga gcaagatctt      1008
110 gtctccacta aatgagctcc tgcggggagta gttggaaagt tggaaccgtg tccagcacag      1068
112 aaggaatctg tgcagatgag cagtcacact gttactccac agcggaggag accagctcag      1128
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116 ctccaccaga gcccatgctc aaccactgtg gcgttctgct gccctgcag ttggcagaaa      1248
118 ggatgttttt gtccatttc cttggaggcc accgggacag acctggacac tagggtcagg      1308
120 cggggtgctg tgggtggggag aggcattggct ggggtggggg tggggagacc tgggtggccg      1368
122 tgggtccagct cttggccctt gtgtgagttg agtctctctt ctgagactgc taagtggggg      1428
124 cagtgatggt tgccaggacg aattgagata atatctgtga ggtgctgatg agtgattgac      1488
126 acacagcact ctctaaatct tccttgtgag gattatgggt cctgcaattc tacagtttct      1548
128 tactgttttg tatcaaaatc actatctttc tgataacaga attgccaagg cagcgggatc      1608
130 tcgtatcttt aaaaagcagt cctcttattc ctaaggtaat cctattaaaa cacagcttta      1668
132 caacttccat attacaaaaa aaaaaaaaaa aaa      1701
135 <210> SEQ ID NO: 2
136 <211> LENGTH: 256
137 <212> TYPE: PRT
138 <213> ORGANISM: Homo sapiens
140 <400> SEQUENCE: 2
142 Val Asn Gln Ala Pro Glu Cys Arg Phe Gly Gly Gly Ile Leu Gly Pro

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143 1          5          10          15
146 Leu Gly Lys Arg Arg Asp Leu Ala Arg Ala Ser Glu Pro Arg Thr Glu
147          20          25          30
150 Gly Ala Arg Arg Ala Gly Pro Gln Pro Arg Pro Leu Ala Asp Pro Ala
151          35          40          45
154 Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser Ser Leu Ser
155          50          55          60
158 Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly Arg Val Val
159 65          70          75          80
162 Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu Phe Ser Met
163          85          90          95
166 Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu Leu Leu Arg
167          100          105          110
170 Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg Arg Val Asp
171          115          120          125
174 Asp Phe Glu Ala Gly Ala Ala Ala Gly Ala Ala Pro Gly Glu Glu Asp
175          130          135          140
178 Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly Lys Asp Trp
179 145          150          155          160
182 Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys Ile Asp Ser
183          165          170          175
186 Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val Arg Glu Ser
187          180          185          190
190 Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr Val Ala His
191          195          200          205
194 Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val Ala Asp Leu
195          210          215          220
198 Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg Ser Gly Ala
199 225          230          235          240
202 Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser Glu Ala Ser
203          245          250          255

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VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date